

## SEQUENCE LISTING

<110> Donna T. Ward  
Andrew T. Watt

<120> ANTISENSE MODULATION OF RIBONUCLEASE L EXPRESSION

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tcaaggaaaa ggctaaaagt ggtagcaggt ggcattttacc gtc atg gag agc agg 115

Met Glu Ser Arg

1

gat cat aac aac ccc cag gag gga ccc acg tcc tcc agc ggt aga agg 163

Asp His Asn Asn Pro Gln Glu Gly Pro Thr Ser Ser Ser Gly Arg Arg

5

10

15

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gct gca gtg gaa gac aat cac ttg ctg att aaa gct gtt caa aac gaa 211

Ala Ala Val Glu Asp Asn His Leu Leu Ile Lys Ala Val Gln Asn Glu

25

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gat gtt gac ctg gtc cag caa ttg ctg gaa ggt gga gcc aat gtt aat 259

Asp Val Asp Leu Val Gln Gln Leu Leu Glu Gly Gly Ala Asn Val Asn

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ttc cag gaa gag gaa ggg ggc tgg aca cct ctg cat aac gca gta caa 307

Phe Gln Glu Glu Glu Gly Gly Trp Thr Pro Leu His Asn Ala Val Gln

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60

65

atg agc agg gag gac att gtg gaa ctt ctg ctt cgt cat ggt gct gac 355

Met Ser Arg Glu Asp Ile Val Glu Leu Leu Leu Arg His Gly Ala Asp

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75

80

cct gtt ctg agg aag aag aat ggg gcc acg cct ttt atc ctc gca gcg 403

Pro Val Leu Arg Lys Lys Asn Gly Ala Thr Pro Phe Ile Leu Ala Ala

85

90

95

100

att gcg ggg agc gtg aag ctg ctg aaa ctt ttc ctt tct aaa gga gca 451

Ile Ala Gly Ser Val Lys Leu Leu Lys Leu Phe Leu Ser Lys Gly Ala

105

110

115

F02T60/629460

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Asp Val Asn Glu Cys Asp Phe Tyr Gly Phe Thr Ala Phe Met .Glu Ala	
120 125 130	
gct gtg tat ggt aag gtc aaa gcc cta aaa ttc ctt tat aag aga gga	547
Ala Val Tyr Gly Lys Val Lys Ala Leu Lys Phe Leu Tyr Lys Arg Gly	
135 140 145	
gca aat gtg aat ttg agg cga aag aca aag gag gat caa gag cgg ctg	595
Ala Asn Val Asn Leu Arg Arg Lys Thr Lys Glu Asp Gln Glu Arg Leu	
150 155 160	
agg aaa gga ggg gcc aca gct ctc atg gac gct gct gaa aaa gga cac	643
Arg Lys Gly Gly Ala Thr Ala Leu Met Asp Ala Ala Glu Lys Gly His	
165 170 175 180	
gta gag gtc ttg aag att ctc ctt gat gag atg ggg gca gat gta aac	691
Val Glu Val Leu Lys Ile Leu Leu Asp Glu Met Gly Ala Asp Val Asn	
185 190 195	
gcc tgt gac aat atg ggc aga aat gcc ttg atc cat gct ctc ctg agc	739
Ala Cys Asp Asn Met Gly Arg Asn Ala Leu Ile His Ala Leu Leu Ser	
200 205 210	
tct gac gat agt gat gtg gag gct att acg cat ctg ctg ctg gac cat	787
Ser Asp Asp Ser Asp Val Glu Ala Ile Thr His Leu Leu Leu Asp His	
215 220 225	
ggg gct gat gtc aat gtg agg gga gaa aga ggg aag act ccc ctg atc	835
Gly Ala Asp Val Asn Val Arg Gly Glu Arg Gly Lys Thr Pro Leu Ile	
230 235 240	
ctg gca gtg gag aag aag cac ttg ggt ttg gtg cag agg ctt ctg gag	883
Leu Ala Val Glu Lys Lys His Leu Gly Leu Val Gln Arg Leu Leu Glu	
245 250 255 260	
caa gag cac ata gag att aat gac aca gac agt gat ggc aaa aca gca	931
Gln Glu His Ile Glu Ile Asn Asp Thr Asp Ser Asp Gly Lys Thr Ala	
265 270 275	
ctg ctg ctt gct gtt gaa ctc aaa ctg aag aaa atc gcc gag ttg ctg	979
Leu Leu Leu Ala Val Glu Leu Lys Leu Lys Lys Ile Ala Glu Leu Leu	
280 285 290	

tgc aaa cgt gga gcc agt aca gat tgt ggg gat ctt gtt atg aca gcg	1027
Cys Lys Arg Gly Ala Ser Thr Asp Cys Gly Asp Leu Val Met Thr Ala	
295 300 305	
agg cgg aat tat gac cat tcc ctt gtg aag gtt ctt ctc tct cat gga	1075
Arg Arg Asn Tyr Asp His Ser Leu Val Lys Val Leu Leu Ser His Gly	
310 315 320	
gcc aaa gaa gat ttt cac cct cct gct gaa gac tgg aag cct cag agc	1123
Ala Lys Glu Asp Phe His Pro Pro Ala Glu Asp Trp Lys Pro Gln Ser	
325 330 335 340	
tca cac tgg ggg gca gcc ctg aag gat ctc cac aga ata tac cgc cct	1171
Ser His Trp Gly Ala Ala Leu Lys Asp Leu His Arg Ile Tyr Arg Pro	
345 350 355	
atg att ggc aaa ctc aag ttc ttt att gat gaa aaa tac aaa att gct	1219
Met Ile Gly Lys Leu Lys Phe Phe Ile Asp Glu Lys Tyr Lys Ile Ala	
360 365 370	
gat act tca gaa gga ggc atc tac ctg ggg ttc tat gag aag caa gaa	1267
Asp Thr Ser Glu Gly Gly Ile Tyr Leu Gly Phe Tyr Glu Lys Gln Glu	
375 380 385	
gta gct gtg aag acg ttc tgt gag ggc agc cca cgt gca cag cgg gaa	1315
Val Ala Val Lys Thr Phe Cys Glu Gly Ser Pro Arg Ala Gln Arg Glu	
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gtc tct tgt ctg caa agc agc cga gag aac agt cac ttg gtg aca ttc	1363
Val Ser Cys Leu Gln Ser Ser Arg Glu Asn Ser His Leu Val Thr Phe	
405 410 415 420	
tat ggg agt gag agc cac agg ggc cac ttg ttt gtg tgt gtc acc ctc	1411
Tyr Gly Ser Glu Ser His Arg Gly His Leu Phe Val Cys Val Thr Leu	
425 430 435	
tgt gag cag act ctg gaa gcg tgt ttg gat gtg cac aga ggg gaa gat	1459
Cys Glu Gln Thr Leu Glu Ala Cys Leu Asp Val His Arg Gly Glu Asp	
440 445 450	
gtg gaa aat gag gaa gat gaa ttt gcc cga aat gtc ctg tca tct ata	1507
Val Glu Asn Glu Glu Asp Glu Phe Ala Arg Asn Val Leu Ser Ser Ile	
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gat ctg caa cca caa aac atc tta ata gat tct aag aaa gct gct cac	1603
Asp Leu Gln Pro Gln Asn Ile Leu Ile Asp Ser Lys Lys Ala Ala His	
485 490 495 500	
ctg gca gat ttt gat aag agc atc aag tgg gct gga gat cca cag gaa	1651
Leu Ala Asp Phe Asp Lys Ser Ile Lys Trp Ala Gly Asp Pro Gln Glu	
505 510 515	
gtc aag aga gat cta gag gac ctt gga cgg ctg gtc ctc tat gtg gta	1699
Val Lys Arg Asp Leu Glu Asp Leu Gly Arg Leu Val Leu Tyr Val Val	
520 525 530	
aag aag gga agc atc tca ttt gag gat ctg aaa gct caa agt aat gaa	1747
Lys Lys Gly Ser Ile Ser Phe Glu Asp Leu Lys Ala Gln Ser Asn Glu	
535 540 545	
gag gtg gtt caa ctt tct cca gat gag gaa act aag gac ctc att cat	1795
Glu Val Val Gln Leu Ser Pro Asp Glu Glu Thr Lys Asp Leu Ile His	
550 555 560	
cgt ctc ttc cat cct ggg gaa cat gtg agg gac tgt ctg agt gac ctg	1843
Arg Leu Phe His Pro Gly Glu His Val Arg Asp Cys Leu Ser Asp Leu	
565 570 575 580	
ctg ggt cat ccc ttc ttt tgg act tgg gag agc cgc tat agg acg ctt	1891
Leu Gly His Pro Phe Phe Trp Thr Trp Glu Ser Arg Tyr Arg Thr Leu	
585 590 595	
cgg aat gtg gga aat gaa tcc gac atc aaa aca cga aaa tct gaa agt	1939
Arg Asn Val Gly Asn Glu Ser Asp Ile Lys Thr Arg Lys Ser Glu Ser	
600 605 610	
gag atc ctc aga cta ctg caa cct ggg cct tct gaa cat tcc aaa agt	1987
Glu Ile Leu Arg Leu Leu Gln Pro Gly Pro Ser Glu His Ser Lys Ser	
615 620 625	
ttt gac aag tgg acg act aag att aat gaa tgt gtt atg aaa aaa atg	2035
Phe Asp Lys Trp Thr Thr Lys Ile Asn Glu Cys Val Met Lys Lys Met	
630 635 640	

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Asn Lys Phe Tyr Glu Lys Arg Gly Asn Phe Tyr Gln Asn Thr Val Gly  
645 650 655 660

gat ctg cta aag ttc atc cgg aat ttg gga gaa cac att gat gaa gaa 2131  
Asp Leu Leu Lys Phe Ile Arg Asn Leu Gly Glu His Ile Asp Glu Glu  
665 670 675

aag cat aaa aag atg aaa tta aaa att gga gac cct tcc ctg tat ttt 2179  
Lys His Lys Lys Met Lys Leu Lys Ile Gly Asp Pro Ser Leu Tyr Phe  
680 685 690

cag aag aca ttt cca gat ctg gtg atc tat gtc tac aca aaa cta cag 2227  
Gln Lys Thr Phe Pro Asp Leu Val Ile Tyr Val Tyr Thr Lys Leu Gln  
695 700 705

aac aca gaa tat aga aag cat ttc ccc caa acc cac agt cca aac aaa 2275  
Asn Thr Glu Tyr Arg Lys His Phe Pro Gln Thr His Ser Pro Asn Lys  
710 715 720

cct cag tgt gat gga gct ggt ggg gcc agt ggg ttg gcc agc cct ggg 2323  
Pro Gln Cys Asp Gly Ala Gly Gly Ala Ser Gly Leu Ala Ser Pro Gly  
725 730 735 740

tgc tga tggactgatt tgctggagtt caggggaacta cttattagct gtagagtcct 2379  
Cys

tggcaaatca caacattctg ggccttttaa ctcaccaggt tgcttgtgag ggatgagttg 2439

catagctgat atgtcagtc cctggcatcgt gtattccata tgtctataac aaaagcaata 2499

tatacccaga ctacactagt ccataagctt taccactaa ctgggaggac attctgctaa 2559

gattcctttt gtcaattgca ccaaaagaat gagtgccttg acccctaatt ctgcatatgt 2619

tacaattctc tcaacttaatt ttcccaatga tcttgcaaaa cagggattat catccccatt 2679

taagaactga ggaacctgag actcagagag tgtgagctac tggccaaga ttattcaatt 2739

tataacctagc actttataaa tttatgtggt gttattggta cctctcattt gggcacctta 2799

aaacttaact atcttccagg gctcttccag atgaggccca aaacatatat aggggttcca 2859

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F02T60-6294560

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F02F50" 6294660



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tcatactgct gatctgttgc cataaaatcc caatttacac tcaaagcttc tttgattaag 180

tgctaagaga taaatttgca ttttctcaag gaaaatcgct aaaagtggta gcaggtggca 240

tttaccgtca tggagagcat aggatcataa caacccccag gagggaccca cgtcctccag 300

cggtagaagg gctgcagtgg aagacaatca cttgctgatt aaagctgttc aaaacgaaga 360

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aggggggctgg acacctctgc ataacgc 447

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